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OM protein - protein search, using sw model	NADH dehydrogenase	31	99.5	4.2	452	2	C71391
Run on:	NADH dehydrogenase	32	98	4.2	348	2	T12280
Title: US-09-455-486-6	NADH dehydrogenase	33	98	4.2	348	2	T12281
Sequence: 1 MESTISMMGSPKSLSETCLPN.....ALVLPSTIVLDLQLCRYPD 454	probable transport	34	98	4.2	442	2	G71940
Scoring table: BLOSUM62	hypothetical prote	35	98	4.2	962	2	T05945
Gapop 10.0 , Gapext 0.5	genome polyprotein	36	98	4.2	3411	1	GNWYV
Searched: 195891 seqs, 67900655 residues	genome polyprotein	37	98	4.2	3411	1	GNWYV
Total number of hits satisfying chosen parameters: 195891	hypothetical prote	38	97.5	4.1	268	2	A70417
Minimum DB seq length: 0	follicle stimulati	39	97.5	4.1	695	2	I45896
Maximum DB seq length: 2000000000	NADH dehydrogenase	40	97	4.1	346	2	T11395
Post-processing: Minimum Match 0%	probable oxidoreductase [imported] - Streptomyces coelicolor	41	97	4.1	348	2	T12283
Maximum Match 100%	C;Species: Streptomyces coelicolor	42	97	4.1	692	2	A34548
Database : PIR_66.*	C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000	43	96.5	4.1	608	2	G02640
1: pir1:*	C;Accession: T50571	44	96.5	4.1	686	2	S30075
2: pir2:*	A;Title: A set of ordered comids and a detailed genetic and physical map for the 8 M.	45	96.5	4.1	711	2	T25281.
3: pir3:*	A;Reference number: 220556; MUID:97000351						
4: pir4:*	A;Accession: T50571						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	A;Molecule type: DNA						
	A;Residues: 1-239 <RED>						
	A;Cross-references: EMBL:ALL133220; PIDN:CAB61708_1						
	A;Experimental source: strain A3(2)						
	C;Genetics:						
	A;Note: SCC75A..0BC						
	C;Superfamily: conserved hypothetical protein MJ1501						
RESULT 1							
T50571							
probable oxidoreductase [imported] - Streptomyces coelicolor							
C;Species: Streptomyces coelicolor							
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000							
C;Accession: T50571							
R;Redenbach, M.; Kieser, H.M.; Denapaitre, D.; Elchner, A.; Cullum, J.; Kinashi, H.; H. Mol. Microbiol. 21: 77-96, 1996							
A;Title: A set of ordered comids and a detailed genetic and physical map for the 8 M.							
A;Reference number: 220556; MUID:97000351							
A;Accession: T50571							
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A;Note: SCC75A..0BC							
C;Superfamily: conserved hypothetical protein MJ1501							
RESULT 1							
T50571							
probable oxidoreductase [imported] - Streptomyces coelicolor							
C;Species: Streptomyces coelicolor							
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000							
C;Accession: T50571							
R;Redenbach, M.; Kieser, H.M.; Denapaitre, D.; Elchner, A.; Cullum, J.; Kinashi, H.; H. Mol. Microbiol. 21: 77-96, 1996							
A;Title: A set of ordered comids and a detailed genetic and physical map for the 8 M.							
A;Reference number: 220556; MUID:97000351							
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C;Genetics:							
A;Note: SCC75A..0BC							
C;Superfamily: conserved hypothetical protein MJ1501							
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Best Local Similarity 27.9%; Pred. No. 3.5e-05; Matches 61; Conservative 41; Mismatches 72; Indels 45; Gaps 10;							
Qy 25 IKDARKVTGVVI-GSGDFAKSLTIRLGYHVYIGSR--NPKFASSEFPHVYDVTHHE 80							
Db 23 LPDVSGLVYVGVLGEGPQQRGLAYRLAKAQKVTVGSRAERAARAAAEEIGHGVEGADNA 82							
Qy 81 DALIKTNITVFAIRE-HVTSILWDLRHLVKGKILDVSNMNRINQ----YPE-SNAE 131							
Db 83 ETARRSDVTVAVAPWDGHSKTLIESRALESKGKLVYVDVCPMLGFDKKGAYALKPEGSAAE 142							
Qy 132 YLASLFPDSLIVKGPNVVAWALO-----LGPKDASRQVYICSNNTIQAROQY 178							
Db 143 QAAALLPDSRVAAFHLSAVLQDPEIDTDVWLVGBERADVEI----vQA--- 192							
Qy 179 IELARQLNFTIP----IDLGSSSARETENPLRLFLTLWR 213							
Db 193 --LAGR--IPGMRCVFAASRLRNAHQVESLYANLISVNR 226							
RESULT 2							
H69410							
conserved hypothetical protein AF1209 - Archaeoglobus fulgidus							
C;Species: Archaeoglobus fulgidus							
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999							
C;Accession: H69410							
R;Klenk, H.-P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchem, K.A.; Dod							
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.							
Gloedek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.F.; Weidman, J.F.; McDonald, L.							
Nature 390, 364-370, 1997							

A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.	Smith, H.O.; Woese, C.R.; Venter, J.C.;	A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Accession: H69400	A; Status: complete genome sequence of the hyperthermophilic, sulfate-reducing archaea	A; Reference number: A69250; MUID:98049343
A; Residues: 1-213 <KLE>	A; Cross-references: GB:AE001021; GB:AE00782; NID:92689344; PIDN:AAB90038.1; PID:g264937	A; Superfamily: conserved hypothetical protein MJ1501
Query Match Score 6.3%; Best Local Similarity 27.5%; Matches 56; Conservative Matches 44; Gaps 11;	Score 147; Pred. No. 0.00017; Mismatches 68; Indels 36;	Length 213;
Qy 37 GSGDFAKSLTIRLJRCGYHVVGSRN-----PKFASEEFFPHVVDVT----HHEDALTNTI 88 Db 8 GTGNLKGGLALRQKLGLEYIVGSRKLEAKELASDYLKVGDASLIGRNEDAETCD- 66	Qy 89 IVAIHRHHTSMLD-----LRHLLVGKILID-----VSNNMNRQNOYPE-SNAE 131 Db 67 --VAV-----FTIPWEFADTAEMIKRQLAGKVVISPLVPMKKVGDNF-YVRPPEGSAE 119	Qy 132 YLASLFPSLIVKGENVYSAWALQLGPKDASROVYICCSNNIQAROOVIELARQINFI-PI 190 Db 120 KIASVLEESSVVAAYHSIPIARRFANLGEEFWDVPICGDS-GAKEVVVDTKEISKGLRLR 178
Qy 191 DLSGLSSARETENL-PLRFLTLWR 213 Db 179 DAGGLSNAHLVESLTPLTINVMKR 202	Qy 3 D69361 conserved hypothetical protein AF08992 - Archaeoglobus fulgidus C; Species: Archaeoglobus fulgidus C; Accession: D69361 R; Kleink, R.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L., Nature 390, 364-370, 1997	Qy 89 IVAIHRHHTSMLD-----LRHLLVGKILID-----VSNNMNRQNOY-PESNAEYLASLFPDSL 143 Db 68 AVLTIPHEAHITARDKNNLRRKIVSPLVPSRGANGTYSSERSAETIVAVLESSR 127
A; Status: preliminary; nucleic acid sequence not shown; translation not shown	A; Status: preliminary; nucleic acid sequence not shown; translation not shown	A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecular type: DNA	A; Molecular type: DNA	A; Molecular type: DNA
A; Residues: 1-212 <KLE>	A; Residues: 1-212 <KLE>	A; Residues: 1-212 <KLE>
C; Superfamily: conserved hypothetical protein MJ1501	C; Superfamily: conserved hypothetical protein MJ1501	C; Superfamily: conserved hypothetical protein MJ1501
Query Match Score 6.0%; Best Local Similarity 25.4%; Matches 49; Conservative Matches 44; Gaps 6;	Score 142; Pred. No. 0.00043; Mismatches 84; Indels 16;	Length 212;
Qy 37 GSGDFAKSLTIRLJRCGYHVVGSRN-----PKFASEEFFPHVVDVT----HHEDALTNTI 88 Db 8 GTGNLKGGLALRQKLGLEYIVGSRKLEAKELASDYLKVGDASLIGRNEDAETCD- 67	Qy 89 IVAIHRHHTSMLD-----LRHLLVGKILID-----LIDVSNMNRQNOY-PESNAEYLASLFPDSL 141 Db 128 VVSALHTPAARFANLGEEFWDVPICGDS-GAKEVVVDTKEISKGLRLSNSRL 187	Qy 142 IVKGENVYSAWALQLGPKDASROVYICCSNNIQAROOVIELARQINFI-PIDLSSSARE 200 Db 201 LENLPRLTLWR 213

Db	8	GTCGQGCGCLALRAK -NNKIIIGSRKEKEAAKAKAKEIILFGRGIADEIGLENKDAAK	66	A; Molecule type: DNA A; Residues: 1-216 <TAK> A; Cross-references: EMBL:AB010203; NID:92780763; PIDN:BAA24368.1; PIDN:g2780765 A; Experimental source: strain Ictero No.1; substrate in icterohaemorrhiae
Qy	85	KTNLIFYAIHREH-YTSLIWDLRHLVGKILIDY-----SNMRINQPE-SNAEYL	133	
Db	67	EGDVVILSLPYETLSTIKOLKEELKGKIVVSVGGVPLATAIGDKPTRLLFPDGSAEMV	126	
Qy	134	ASLFPDSSLVKGFFNNTSYAWALOLGPGRDASRQYICCSNNIQAROOVIELARQLNFI-PIDL	192	Query Match Score 5.1%; Best Local Similarity 23.7%; Matches 47; Conservative Matches 47; Mismatches 91; Indels 23; Gaps 6;
Db	127	QNVLKESKEVSAFQNYCHAVELLDLNPVDCDLVLCGNDNEAKKVVIDLANQIDVRAIDC	186	
Qy	193	GSLSKAREIENLPLRLFTLWLRGPVVAISL 222	99	Query Match Score 5.1%; Best Local Similarity 23.7%; Matches 47; Conservative Matches 47; Mismatches 91; Indels 23; Gaps 6;
Db	187	GNLEKSRIEAIT-----PLIGLNI 207	99	
RESULT	6			
A69131	conserved hypothetical protein MT248 - Methanobacterium thermoautotrophicum (strain Del C; Species: Methanobacterium thermoautotrophicum C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999 C; Accession: A69131 R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7135, 1997 A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID:9803514 A; Accession: A69131 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-232 <MTB> A; Cross-references: GB:AE000811; GB:AE000666; NID:g2621287; PIDN:AAB84754.1; PIDN:g262129 A; Experimental source: strain Delta H C; Genetics:			
A; Gene: MT248 A; Start codon: TTT C; Superfamily: conserved hypothetical protein MJ1501				
RESULT	8			
G82642	conserved hypothetical protein XFI137 [imported] - Xylella fastidiosa (strain 9c) C; Species: Xylella fastidiosa C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C; Accession: G82642 R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 40(6), 151-157, 2000 A; Title: The genome sequence of the plant pathogen Xylella fastidiosa. A; Reference number: A82515; MUID:20365717 A; Note: for a complete list of authors see reference number A593328 below A; Accession: G82642 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-242 <CSM> A; Cross-references: GB:AE003997; GB:AE003849; NID:99106805; PIDN:AAF84546.1; GS A; Experimental source: strain 9ac C; Authors: Ferreira, V.C.A.; Fraga, J.A.; Franco, S.C.; Krieger, J.E.; Kuramae, E.L.; Marinho, C.L.; Marques, M.V.; Menck, C.F.M.; Miraces, E.C.; Miyazaki, H.M.P.; Marin, C.; Oliveira, R.C.; Palmeira, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Chado, M.A.; Madeira, A.M.B.N.; Madeira, A.M.B.N.; Matsuura, A.Y.; Menck, C.F.M.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; Santelli, R.V.; Santos, M.; Tsuhako, M.H.; Vallada, H.; da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; de M.; Tsuhako, M.H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore A; Reference number: A593328 A; Contests: annotation C; Genetics:			
A; Gene: XFI137				
RESULT	7			
T00121	hypothetical protein 8 - Leptospira interrogans C; Species: Leptospira interrogans C; Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000' C; Accession: T00121 R; Takahashi, Y.; Akase, K.; Hirano, H.; Fukunaga, M. Gene 215, 37-45, 1998 A; Title: Physical and genetic maps of the Leptospira interrogans serovar ictero haemorrhiae A; Reference number: 214115; MUID:98332717 A; Accession: T00121 A; Status: preliminary; translated from GB/EMBL/DBJ			
Qy	187	FI-PIDLGSLSKAREIENLPLRLFTLWLRGPVVAISL 211	89	Query Match Score 5.0%; Best Local Similarity 24.0%; Matches 46; Conservative Matches 46; Mismatches 40; Indels 21; Gaps 7;
Db	187	GYRAIECGGLENLARIEKTPLLNL 212	89	
RESULT	7			
T00121	hypothetical protein 8 - Leptospira interrogans C; Species: Leptospira interrogans C; Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000' C; Accession: T00121 R; Takahashi, Y.; Akase, K.; Hirano, H.; Fukunaga, M. Gene 215, 37-45, 1998 A; Title: Physical and genetic maps of the Leptospira interrogans serovar ictero haemorrhiae A; Reference number: 214115; MUID:98332717 A; Accession: T00121 A; Status: preliminary; translated from GB/EMBL/DBJ			
Qy	28	ARKTVGIGSGDFAKSLTIRLIRGCVYHVGSRNPFASEFFPHVVDYTHHEDAL 83	83	Query Match Score 5.0%; Best Local Similarity 24.0%; Matches 46; Conservative Matches 46; Mismatches 40; Indels 21; Gaps 7;
Db	30	AAPMRIGVIGAGSLGTLVKGHEVMSSRNPDPKLEMARELPR-ASVGQPLAAT 88	88	
Qy	84	TKTNLIFVAAIREHYTSWL-DLRHLYVKILIDVSNMNRINQ---YPSIN---AEYLAS 135	148	
Db	89	EFGTIVVLLAPPFEAALPOVGRDERSAYRKIVTDSTPVGASSADVREARELGVACTVYK 148	148	

Qy	136 LFPDSLIVKGFFNVVSARALQGLPKDASRQ-----VYICSNNIQARQVIELARQLNFIPI 190	Qy	307 -----LLSFFFAMVHVA-----YSCLCPMRSERVLFLNMAAQOQHANIENS 348
Db	149 YMGRARLYRAFSAVDATVVE---TSASRRGGGIGMPLASDDAEAMKVAEGLIVRDAGCDPV 205	Db	362 YNLRLWIFISLATAIGNIVIVLTTTSQYKLTVP----RFLMCNLAFAD----- 408
Qy	191 DLGSLSSEAREIE 202	Qy	349 WNEEEVWRIEMYTSFGIMSGLISLIAVTSTPSVSNALNWR-----FSFIQSTLG 399
Db	206 IVGNLAAASFQ 217	Db	409 -----LCIGIYLILIASDVIHTKSQYHNIAIDWQTGAGCDAAGFTVASELS 456
RESULT 9	JN0988	Qy	400 ---YVALLISTH-----VLIYGMKRAFEEYYRFYIPPNFV-LAL 436
	folliotropin receptor precursor - crab-eating macaque	Db	457 VYLTATLTERHTITHAMQLDCVKHVRHAASVMNGWFAFAAALPPIFGISSYMKVSI 516
N: Alternative names: follicle-stimulating hormone receptor (FSHR)	C:Species: Macaca fascicularis (crab-eating macaque)	Qy	437 VLPSTIVIDLQL 449
C:Accession: JN0988; S30452	R:stromoli, J.; Dankbar, B.; Sharma, R.S.; Nieschlag, E.	Db	517 CLPMDIDSPLSQL 529
A:Title: Molecular cloning of the testicular follicle stimulating hormone receptor of th	A:Reference number: JN0988; MUID:94071854	RESULT 10	S59681
A:Molecule type: mRNA	A:Accession: JN0988		probable membrane protein YPL012w - yeast (Saccharomyces cerevisiae)
A:Residues: 1-695 <GRO>	A:Keywords: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat		N: Alternate names: hypothetical protein YPA5w; hypothetical protein YP8132_01
A:Cross-references: ENBL:X74454; NID:9396801; PIDN:CAA52463.1; PID:9396802	C:Species: Saccharomyces cerevisiae		C:Species: Saccharomyces cerevisiae
A:Note: the authors translated the codon AGT for residue 488 as Arg	C:Accession: S59681; S52519		C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 12-Dec-1997
C:Function:	A:Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friessen, J.D.; Storms, R.K.; Vo, D.H.; submitted to the EMBL Data Library, August 1995		C:Accession: S59681; S52519
A:Description: receptor that mediates the biochemical effects of follitropin	A:Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.		A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat	A:Accession: S59681		A:Experimental source: strain AB972
C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; phosphoprotein;	A:Residues: 1-1228 <IRL>		A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w
F: 1-8-695/Product: follitropin receptor #status predicted <SIG>	A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w		A:Experimental source: strain AB972
F: 71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>	A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w		A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w
F: 121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>	A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w		A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w
F: 146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>	A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w		A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w
F: 172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>	A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w		A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w
F: 194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>	A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w		A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w
F: 367-387/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>	A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w		A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w
F: 444-465/Domain: transmembrane #status predicted <TM2>	A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w		A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w
F: 486-508/Domain: transmembrane #status predicted <TM3>	A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w		A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w
F: 574-597/Domain: transmembrane #status predicted <TM4>	A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w		A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w
F: 609-610/Domain: transmembrane #status predicted <TM6>	A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w		A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w
F: 755/Binding site: carbohydrate (Asn) (covalent) #status predicted <TM7>	A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w		A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w
F: 596/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted <TM8>	A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w		A:Cross-references: ENBL:U33335; NID:9965076; PID:9365081; MIPS:YPL012w
Query Match 4.7%; Score 111.5; DB 1; Length 695;	Query Match 4.7%; Score 111.5; DB 2; Length 1228;		
Best Local Similarity 17.0%; Pred. No. 0..5; Mismatches 151; Indels 183; Gaps 16;	Best Local Similarity 19.9%; Pred. No. 1; Matches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 28;		
Matches 84; Conservative 75; Mismatches 151; Indels 183; Gaps 16;			
Qy 79 HEDALTKTNAIYAHREHYTLSDWLRHLLVG-----KILDVSNNMR 121	Qy 11 KSLSETCLPGINGIRDARK-----VTVGVIGSGDPAKSLSIRL 50		
Db 98 INQPESSNAEYLASLFPDSLIVKGFFNVVSANALQGLPKDASRQVTCNSNIIQARQVIEL 181	Db 292 KTMATTISGLAENKYLRVLDTIFALKPSNVDTLLTKSWIAVIGKMSYATHQPLKAL 351		
Db 157 IH-----TIENSFWLSEFSLWL-----NKNGIQEIHNC 189			
Qy 182 ARQLNFIPIDGSLSSAREIEULPLRLETFLWRGPVVVAISLATEFFLYSFVRDVHPIYAR 241	Qy 51 R-----CGYHVIGSGDPAKSLSIRL 51		
Db 190 --FNGTOLDDELNSDNINNLSEELPNDFHGASGPVILLDISRTIHSUPSYGENLKKLA 246	Db 352 RKIPGVPHIMCTY--LASPEPEVYQAQSCLISLSEVKDLILYTPSYDEKFKNVD 408		
Qy 242 NQSDFVKYKIPIEVNKTLPVATLSSLV-----271	Qy 84 -----TKTNLILFVATHREHYTLSDLRHLVKGKILDSNNMRINQYESNAEYLASL 137		
Db 247 RSTYNLKLP-----SLEKVALMEASLTYPSSHCCAFANWRQRQISELHPICNKSILRQE 301	Db 409 EITISQIATFIDFLSRYSHCS---REIL-KILVAFFKFRY ---RSNPHEFLKL 456		
Qy 272 -----LAGLLAAAYQOLYYGTKYRRE-----PPWLETWQLCRKQLG 306	Qy 138 PDSLIVKGFFNVVSALOLQPKDASRQVYIGSNNIQARQVTELARQLNFT-----188		
Db 302 DYMTOQRGQRSSLAEDNESSYSRGFDMTYAEDYDLCNEVVDDTCSPKDRAFTCPCDILG 361	Db 457 -----KIVDTWRYN-----EQPMDLRNIELEYVIGASISAMG 488		
Qy 189 -----PIDIGSLSARETENLPURLFTRWGPV-----VAISLATEFLYFLSPYRDI 236	Qy 489 PEMILAEAPLNLDNPSSER----PGR -AWLPLIRDTKMANLATF-----QNEL 533		

Qy 237 HPYARNOQSDFYKIPIEVNH-----TKLPP-----IVAITLSSL 269	Db 189 ----ENGTODELNLSDNDNLEELPNDYFHGASGPVILDISRTIHSPLPSYGLENLKKL 243
Db 534 AYPIKSFQSKFDPKYPEESTQLRVEQTIVDQITWSTLPRFCLPMDURESTDEPASELSSL 593	Qy 240 ARNQSDFYKIP-----EIVNKTLPIVAITL 267
Qy 270 VYL-----AGLLAAAYOLYYGTK-----YRFP-----PWLETWLQCRK 303	Db 244 RARSTYNLKKLPTLEKFVTLMEASLTYPHCCAFANWRROISDLRPICKNSILRQEVDTM 303
Db 594 LYSEVELRTTICHALKVLAESNVSYAEESSSHNVNLQRREPSEAQNTEYEST-----K 648	Qy 268 S-----LYVLAGLIAAAYOLYYGTKYRFP-----PPWLETWLQCRKQLG--- 306
Qy 304 QGLLSSFFAMVHAYSLCPLMRS-----ERYL-----FLRMAYQOVHANTENSNE 351	Db 304 TQARQQRVSIAEDGESSLAKREFDPMSEPNYDLCNEVVVICSPKPDAFNPCEDLMGHDI 363
Db 649 STNLAVLFNV----TQTPNASYLETLIDQKLTKTSKEDLEKTFNNVCGLLKNSNE 704	Qy 307 -LLSFFFMVHVA-----YSCLCPMRSERERYLFLMAYQOVHANTENSNE 351
Qy 352 EYVRRIEMTISFGIMSLGLSL-----AVTSGIMSLGLSLNWRREFSTIQTSLGYVALLISTFH 409	Db 364 LRVLIWFISLATAITGNLIELVLVILITSQYKLTVP-----REFMCNLAFTD----- 407
Db 705 ESGGNVNKEKKPKQPLITATLTLICMTIYLPVSSYSALESMSFS-----LTVNSAD 754	Qy 352 EYVRRIEMTISFGIMSLGLSLLLAVTSIPSVSNALNWR-----FSFIQSTLG--- 399
Qy 410 VLIGWKRAFEEEYRFYT 428	Db 408 -----ICIGIYLLASIDITHKSQYHNYAINWOTGCDAAAGFTVFAESLSVYT 458
Db 755 ALIQ--KRA---YRIT 766	Qy 400 YVALLISTFH-----VLIYGWKRAFEEEYRFYTTPNEV-LALVLP 439
RESUL 11	Db 459 LTATLTERWHTITHAMQLCRQVYRHAASIMLYGWIFATVALPIFGSSYMMVSCILP 518
JC4301 folliculin receptor - pig	Qy 440 SIVIDLQL 449
N; Alternate names: follicle-stimulating hormone receptor	Db 519 MDIDSPSQL 528
C; Species: Sus scrofa domestica (domestic pig)	
C; Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 21-Jan-2000,	T28379
C; Accession: JC4301	ORF MSV218 hypothetical protein - Melanoplus sanguinipes entomopoxvirus
R; Reny, J.J.; Lahbib-Mansais, Y.; Bozon, V.; Couture, L.; Pajot, E.; Grebert, Gene 163, 257-261, 1995	C; Species: Melanoplus sanguinipes entomopoxvirus
A; Title: The porcine follitropin receptor: cDNA cloning, functional expression and chromosomal location	C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
A; Reference number: MUID:36011644	C; Accession: T28379
A; Accession: JC4301	J. Virol. 73, 533-552, 1999
A; Residues: 1-694 <REMOVED>	A; Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A; Cross-references: GB:L31966	A; Reference number: Z20484; MUID:99102612
C; Experimental source: ovarian granulosa cells	A; Accession: T28379
C; Comment: This receptor belongs to the family of the G-protein coupled receptors. It has been cloned in male and oogenesis in female.	A; Status: preliminary; translated from GB/EMBL/DDBJ
C; Genes: fshr	A; Molecule type: DNA
A; Map position: 3 q2.2-q2.3	A; Residues: 1-120 <REMOVED>
C; Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat domain	A; Cross-references: EMBL:AF063866; NID: 94049647; PIDN: AAC97747.1; PID: 94049787
C; Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein	C; Genetics:
F; 1-165 /domain: follicle-stimulating hormone binding #status predicted <NOB>	A; Note: Msy218
F; 70-94 /domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>	Query Match 4.6%; Score 109; DB 2; Length 320;
F; 366-388 /domain: transmembrane #status predicted <TM1>	Best Local Similarity 19.3%; Pred. No. 0.3;
F; 398-420 /domain: transmembrane #status predicted <TM2>	Matches 58; Conservative 63; Mismatches 96; Gaps 13;
F; 443-464 /domain: transmembrane #status predicted <TM3>	Qy 16 TC--LPNGINGIKOARKVTVGVIGSGDFAKSLTRLRCGTVHVGSRNPKFASEFFPH 72
F; 485-507 /domain: transmembrane #status predicted <TM4>	Db 10 TCSQVINTNPLVYKOKSVCT-----IKHKNYKKILCENYHLFNKRNIAK--KYFDY 59
F; 528-549 /domain: transmembrane #status predicted <TM5>	Qy 73 VVDVTHHEDALTKTNLIFV-----ATREHHTSLWDRHLVKGRLIDVSN 119
F; 572-596 /domain: transmembrane #status predicted <TM6>	Db 60 ILKNIFPK-LSLESIYVNNELSKYINHLEVYREYTKL-----LNSNELDENHN 111
F; 608-629 /domain: transmembrane #status predicted <TM7>	Qy 120 MRINQYPESENAYLASLFPDSLIVKGFNNVYSAWALQLGPKDASR-----163
Query Match 4.7%; Score 110.5; DB 2; Length 694;	Db 112 LWINYLKSTYSEYNNTDFNNIKLQLENPKILDNIPNDHKSGILFKKNITYNKKPN 171
Best Local Similarity 16.5%; Pred. No. 0.6;	Qy 164 QVYI-----CSNNIQARQVIELARQLNFNIPIDGLSLSAREI-ENPL 206
Matches 91; Conservative 90; Mismatches 170; Indels 199; Gaps 20;	Db 172 NIYLLYSGCILIFYNPEKNCSNL--NNIKKEKE--ISIELASILYKKKINYKNICN 224
Qy 18 LPNG-INGIKDARVTVGIVGSGDFAKSLTRLRCGTVHVGSRNPKFASEFFPHVVDY 76	Db 207 RLFTLWRGPVV-----VAISLATEFFFLYFLYSPVDRVHYPYARNQDFKPKIPIELVNT 258
Db 60 IPKGAFSGFGDFDEK-----EISQNDVLETEAN---VFSNLPKL-----96	Qy 120 MRINQYPESENAYLASLFPDSLIVKGFNNVYSAWALQLGPKDASRQVYICSNNIQARQVYI 179
Qy 77 THEDALTKTNLIFVAIHRHRYTSLWDRHLVKG-----KILIDVSN 119.	Db 225 ALIYWKSKKLKVNKYLKILKILEPNTYDEYYFKNDII-YNSNEYDFNFDIYNAIKT 282
Db 97 -HELTERXANNL-LYIDPAQUNPLNRLYLLNTGVKHLPAVHKIQSIQKVLIDION 153	Qy 259 L 259
Qy 154 INIH-----TVERNSFWGMLSFESMILW-----SKNGTIREIHWA-----188	Db 283 L 283
Qy 180 ELAROLNFNIPIDGLSLSAREIENLPLRLWGRGPVVAISLATEFFFLYSPVDRVHYPY 239	

RESULT 13

S50969 probable membrane protein YLL051c - yeast (Saccharomyces cerevisiae)

N: Alternate names: hypothetical protein L093

C: Species: Saccharomyces cerevisiae

C: Date: 11-Feb-1995 #sequence_revision 12-May-1995 #text_change 20-Jun-2000

C: Accession: S50969; S64803

R: Wedler, H.; Wambutt, R.

R: Wedler, H.; Wedler, E.; Schäfer, M.; Wambutt, R.

submitted to the EMBL Data Library, January 1995

A: Description: Sequence of a 37 kb DNA fragment from chromosome XII of Saccharomyces cerevisiae

A: Reference number: S50950

A: Accession: S50969

A: Molecule type: DNA

A: Residues: 1-712 <WED>

A: Cross-references: EMBL:Z47973; NID:9642313; PID:9642333

R: Wedler, H.; Wedler, E.; Schäfer, M.; Wambutt, R.

submitted to the Protein Sequence Database, May 1996,

A: Reference number: S64792

A: Accession: S64803

A: Molecule type: DNA

A: Residues: 1-712 <WEN>

A: Cross-references: EMBL:Z73156; NID:91360252; PID:91360253; MIPS:YLL051c

C: Experimental source: strain S288C

C: Genetics:

A: Gene: SGD:FRE6

A: Cross-references: SGD:S0003974; MIPS:YLL051c

A: Map position: 12L

C: Superfamily: ferric reductase FRE2

C: Keywords: transmembrane protein

F: 172-188/Domain: transmembrane #status predicted <TM1>

F: 245-261/Domain: transmembrane #status predicted <TM2>

F: 287-303/Domain: transmembrane #status predicted <TM3>

F: 364-380/Domain: transmembrane #status predicted <TM4>

F: 388-404/Domain: transmembrane #status predicted <TM5>

Query Match 4.6%; Score 109; DB 2; Length 712;

Best Local Similarity 18.8%; Pred. No. 0.82;

Matches 72; Conservative 51; Mismatches 119; Indels 142; Gaps 17;

Db 183 IIAVEFHMHYGNINRALFAESRENVYLRGFVLPFLD---KHAHHEKFVNEVETGL 238

Qy 88 IIIFVAIHRHYTSL-----WDLRLVKGKILIDVSNNMRINOPESNAEYLASL 136

Db 137 FPDLSIVKGDNVYSAWALQLGPKDASRQVYICSNNIQARQVYIELARQNFIPIDLGSLS 196

Db 239 MPDSL-----EAW-----

Qy 197 SAREIENPLRPLTLWRCPVVVAISLATFFFL-YSFYRDVIIHPYARNQSDFYKIPLEIV 255

Db 247 -----LIFCYTLANLIFLISYSLIDPYNLIFNSHLSQTRL---LA 284

Qy 256 NKRLPIAVITLLEVLVLAGLAAQLYGVTKYRFPWLQCKQLGULLSFFFAFMV 315

Db 285 DRS-GILAAFTQFLLITIFTARNSFLELTGVKFNSF-----ISFKWKIGRMVNATI 336

Qy 316 H-VAYSLCLPMMRSERYLFLNNMAYQQVHANIENSWNEEVRIEMYSFGTMSLGLI-SLL 374

Db 337 HSISYSL-----PAIINHAFK-----ISNK-----

Qy 375 AVTSIPSYNALWREFSFIQSTLGVALLI--STPHVLIY-GWKRFAE-----EE 422

Db 374 LVLSLGIYRK---RHKEFFLYTHITLALLFFYCC@HVKLFNGKWEIVVSSLINGLEK 429

Qy .423 YRFYTPPNFVIALVLPBIVLD 446

Db 430 LFHWN---ILQFRPKATLNL 449

RESULT 14

S60385 probable membrane protein YOL152w - yeast (Saccharomyces cerevisiae)

N: Alternative names: hypothetical protein AOB629; hypothetical protein 00443

C: Species: Saccharomyces cerevisiae

C: Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jul-2000

C: Accession: S60385; S66849; S57673

R: Casanayor, A.; Aldea, M.; Casas, C.; Herrero, E.; Gamo, F.J.; Lafuente, M.J.; Gance Yeast 11, 1281-1288, 1995

A;Title: DNA sequence analysis of a 13 kbp fragment of the left arm of yeast chromosome A;Reference number: S60385; MUID:96132030

A;Accession: S60385

A;Molecule type: DNA

A;Residues: 1-629 <CAS>

A;Cross-references: EMBL:Z48239; NID:91163073; PID:CAA88276.1; PID:9886945
R;Arino, J.; Casamayor, A.; Gamo, F.J.; Gancedo, C.; Lafuente, M.J.; Aldea, M.; Casas, C
submitted to the Protein Sequence Database, July 1996

A;Reference number: S66849

A;Accession: S66849

A;Molecule type: DNA

A;Residues: 1-629 <ARI>

A;Cross-references: EMBL:Z74894; NID:91420058; PID:e251928; PID:g1420059; MIPS:YOL152w

A;Experimental source: strain S28C

C;Genetics:

A;Gene: SGD:FRE7

A;Cross-references: SGD:S0005512; MIPS:YOL152w

A;Map position: 15L

C;Keywords: transmembrane protein

F;50-66/Domain: transmembrane #status predicted'<TM1>

F;125-141/Domain: transmembrane #status predicted'<TM2>

F;157-173/Domain: transmembrane #status predicted'<TM3>

F;200-216/Domain: transmembrane #status predicted'<TM4>

F;242-258/Domain: transmembrane #status predicted'<TM5>

F;266-282/Domain: transmembrane #status predicted'<TM6>

F;297-313/Domain: transmembrane #status predicted'<TM7>

Query Match Score 4.6%; Score 107.5; DB 2; Length 629;
Best Local Similarity 21.7%; Pred. No. 0.92; Matches 57; Mismatches 46; Indels 83; Gaps 17;

Matches 57; Conservative 46; Mismatches 77; Indels 83; Gaps 17;

Qy 214 GPVVAISLATAFFFLYSFPRDVHPYARNQQSDFYKIPETIVKNTLPIVATLILSLVV-L 272

Db 123 GFLVVMATTLYTLYCFP--HPFYR-PCAGFRGSPPLSV--RAGIMAISVPFVSL 175

Qy 273 AG -----LLAAAYQLYYGTKYRFPPLWTLQCRKQLGLSFEFMVHVAISLCLPM 325

Db 176 SGKINIVGLVGSTE---KNNYHQ-----ASITCILFFSWVHV----IPF 215

Qy 326 RRSERYLFLNMAKQVHANIENSNEEWRIEMYISFGIMSGLGLSLLAVTSP----- 380

Db 216 LRQARH---EGGYFRMH---QRNKAQDAMWR-----SGVPPPLFLNLMLSSPIARRH 262

Qy 381 --SYSNALAWREFSPHQIQTGLYVALLISTPHV-----LITYGMKRAEEEYFR- 425

Db 263 EYEIFLQLHW---TLAGYGFYISL-----YHVPPELNNSHYLLVATIVVN--PAQLFYRL 311

Qy 426 ---FTYTPPNFVLVLPSPVIL 444

Db 312 AVKGYLRLPORSFMASTIANVSTV 334

Search completed: March 14, 2001, 16:14:04
Job time: 105 sec

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